



SEQUENCE LISTING

<110> Daniel H. Cohn
Muhammad Faiyaz ul Haque
Lily M. King
Deborah Krakow

<120> 3-Phosphoadenosine-5-Phosphosulfate
(PAPS) Synthetase Proteins and Methods for Treating
Osteoarthritic Disorders

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RECEIVED

MAR 07 2003

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| Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr | | |
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| Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp Asn | | |
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| Val Arg His Gly Leu Asn Arg Asn Leu Gly Phe Ser Pro Gly Asp Arg | | |
| 85 90 95 | | |
| Glu Glu Asn Ile Arg Arg Ile Ala Glu Val Ala Lys Leu Phe Ala Asp | | |
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| Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys Asp | | |
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| Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe Phe | | |
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| Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr | | |

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| 180 | 185 | 190 | |
| Lys Thr Asn Leu Ser Thr Val Ser Asp Cys Val His Gln Val Val Glu | | | |
| 195 | 200 | 205 | |
| Leu Leu Gln Glu Gln Asn Ile Val Pro Tyr Thr Ile Ile Lys Asp Ile | | | |
| 210 | 215 | 220 | |
| His Glu Leu Phe Val Pro Glu Asn Lys Leu Asp His Val Arg Ala Glu | | | |
| 225 | 230 | 235 | |
| Ala Glu Thr Leu Pro Ser Leu Ser Ile Thr Lys Leu Asp Leu Gln Trp | | | |
| 245 | 250 | 255 | |
| Val Gln Val Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe Met | | | |
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| Arg Glu Lys Glu Tyr Leu Gln Val Met His Phe Asp Thr Leu Leu Asp | | | |
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| Glu Asp Lys Thr Arg Leu Glu Gly Cys Ser Lys Phe Val Leu Ala His | | | |
| 305 | 310 | 315 | 320 |
| Gly Gly Arg Arg Val Ala Ile Leu Arg Asp Ala Glu Phe Tyr Glu His | | | |
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| Arg Lys Glu Glu Arg Cys Ser Arg Val Trp Gly Thr Thr Cys Thr Lys | | | |
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| His Pro His Ile Lys Met Val Met Glu Ser Gly Asp Trp Leu Val Gly | | | |
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| Gly Asp Leu Gln Val Leu Glu Lys Ile Arg Trp Asn Asp Gly Leu Asp | | | |
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| Gly His Ala Leu Leu Met Gln Asp Thr Cys Arg Arg Leu Leu Glu Arg | | | |
| 420 | 425 | 430 | |
| Gly Tyr Lys His Pro Val Leu Leu His Pro Leu Gly Gly Trp Thr | | | |
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| Lys Asp Asp Asp Val Pro Leu Asp Trp Arg Met Lys Gln His Ala Ala | | | |
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| Val Leu Glu Glu Gly Val Leu Asp Pro Lys Ser Thr Ile Val Ala Ile | | | |
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| Phe Pro Ser Pro Met Leu Tyr Ala Gly Pro Thr Glu Val Gln Trp His | | | |
| 485 | 490 | 495 | |
| Cys Arg Ser Arg Met Ile Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg | | | |
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| Asp Pro Ala Gly Met Pro His Pro Glu Thr Lys Lys Asp Leu Tyr Glu | | | |
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| Pro Thr His Gly Gly Lys Val Leu Ser Met Ala Pro Gly Leu Thr Ser | | | |
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| Val Glu Ile Ile Pro Phe Arg Val Ala Ala Tyr Asn Lys Ala Lys Lys | | | |
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| Ala Met Asp Phe Tyr Asp Pro Ala Arg His Asn Glu Phe Asp Phe Ile | | | |
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| Ser Gly Thr Arg Met Arg Lys Leu Ala Arg Glu Gly Glu Asn Pro Pro | | | |
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610 615

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50 55 60
Glu Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp
65 70 75 80
Asn Val Arg His Gly Leu Asn Lys Asn Leu Gly Phe Ser Ala Gly Asp
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Arg Glu Glu Asn Ile Arg Arg Ile Ala Glu Val Ala Lys Leu Phe Ala
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Asp Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys
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Asp Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe
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Val Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe
165 170 175
Thr Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Cys Val
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Ile His Glu Leu Phe Val Pro Glu Asn Lys Val Asp Gln Ile Arg Ala
225 230 235 240
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Lys His Pro His Ile Lys Met Val Met Glu Ser Gly Asp Trp Leu Val

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| Ile | Phe | Pro | Ser | Pro | Met | Leu | Tyr | Ala | Gly | Pro | Thr | Glu | Val | Gln | Trp |
| | | | | | | 485 | | | | 490 | | | | | 495 |
| His | Cys | Arg | Cys | Arg | Met | Ile | Ala | Gly | Ala | Asn | Phe | Tyr | Ile | Val | Gly |
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| Glu | Pro | Thr | His | Gly | Gly | Lys | Val | Leu | Ser | Met | Ala | Pro | Gly | Leu | Thr |
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| Ser | Val | Glu | Ile | Ile | Pro | Phe | Arg | Val | Ala | Ala | Tyr | Asn | Lys | Ile | Lys |
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| Lys | Ala | Met | Asp | Phe | Tyr | Asp | Pro | Ala | Arg | His | Glu | Glu | Phe | Asp | Phe |
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| accatcaaag | gcatccacga | actctttgt | ccagaaaaaca | aagtgcatca | aatccgagct | 720 |
| gagggcagaga | ctctcccatc | actaccaatt | accaagctgg | atctgcagtg | ggtgcagatt | 780 |
| ctgagtgaag | gctggccac | tcccctcaaa | ggctttatgc | gggagaagga | atacttgcaa | 840 |
| actctacact | tcgacactct | actggacgat | ggagtcatca | acatgagtat | tccattgt | 900 |
| ttgcccgttt | ctgcgatga | caaggcacgg | ctcgaagggt | gcagcaatt | tgccttgatg | 960 |
| tacgaaggtc | ggagggtcgc | tcttattacag | gaccctgaat | tctatgagca | taggaaagag | 1020 |
| gagcgttgtt | ctcgttgtgt | ggggAACAGGC | actgc当地 | acccccc当地 | caaaatggtg | 1080 |
| atgaaagtg | gggactggct | tgttggtgga | gacccatgg | tgcttagagag | aataaggtgg | 1140 |
| gacgatgggc | tggaccaata | ccgccttaacg | cctctggaa | tcaaacagaa | gtgtaaagac | 1200 |
| ataaatgctg | atgcccgtt | tgcattccag | ttgc当地 | ctgtccacaa | tggcatgccc | 1260 |
| ctcctgtatgc | aggacacccg | ccgc当地 | ctggagaggg | tttacaagca | cccaactc | 1320 |
| ctgctccacc | ctctggggg | ctggaccaag | gacgatgacg | tacctctgg | atggaggatg | 1380 |
| aaacagcatg | cagctgtact | ggaggaaagg | gtcctggatc | ccaaactca | tattgttgc | 1440 |
| atctttccat | ctcctatgtt | atacgctgt | cccacagagg | tccactgca | ttgc当地 | 1500 |
| cggatgattt | caggagccaa | tttctacatt | gtgggttaggg | atcccgagg | aatgccccat | 1560 |
| cctgagacaa | agaaaagacct | atatacacc | acccacgggg | gcaaggctt | gagttatggcc | 1620 |
| cctggcctta | cctctgtgga | aataattccg | ttccgagttgg | ctgc当地 | taaaattaaa | 1680 |
| aaggccatgg | acttttatga | tccagcaagg | cacgaggat | ttgacttcat | ctcaggaact | 1740 |
| cgcacatgg | agctgc当地 | ggaaggagaa | gatccccag | atggcttcat | ggccccgaaa | 1800 |
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| cagtgtgttc agtgtgtgtg tgggtgtgtg tgggtgtgtg tgcgtgtgca tgggtgtgtg 180 | | |
| catgtgtgtg tgcgtgtgca tgggtgtgtg ttgaaagata atctgagttt ctttattccc 240 | | |
| tggccaatct cagtaactat tgccaatttc gtttccaca gaacattgta ccccacacca 300 | | |
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<220>
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coding sequence

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<220>
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residues 472 through 477

<400> 31
Asp Pro Lys Ser Thr Ile
1 5

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<220>
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coding sequence with mutation c to a at nucleotide
position +1424

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<220>
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Asp Pro Lys
1

18